

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2005, 22:36:25 ; Search time 46 Seconds
(without alignments)
539,189 Million cell updates/sec

Title: US-09-518-931-2

Perfect score: 1634

Sequence: 1 MRALGGPLSLCLVLALPA.....RVARMPLGSLSVRRFLPVH 300

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgm2_6/ptodata/1/aaa/5 COMB.pap.*
- 2: /cgm2_6/ptodata/1/aaa/6 COMB.pap.*
- 3: /cgm2_6/ptodata/1/aaa/H COMB.pap.*
- 4: /cgm2_6/ptodata/1/aaa/PCTUS COMB.pap.*
- 5: /cgm2_6/ptodata/1/aaa/RE COMB.pap.*
- 6: /cgm2_6/ptodata/1/aaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1634	100.0	300	1	US-08-794-796-2
2	1634	100.0	300	2	US-09-632-277A-2
3	1634	100.0	300	2	US-09-523-323-52
4	1634	100.0	300	2	US-09-896-096A-1
5	1634	100.0	300	2	US-09-936-019-3
6	1634	100.0	333	2	US-09-949-018-7678
7	1619.5	99.1	299	2	US-09-286-529-17
8	1491	91.2	271	2	US-09-936-019-1
9	1177	72.0	211	2	US-09-286-529-20
10	855	52.3	146	2	US-09-523-323-59
11	841	51.5	153	2	US-09-286-529-2
12	465.5	28.5	326	2	US-10-232-858-71
13	465.5	28.5	326	2	US-09-338-063A-71
14	447	27.4	401	2	US-10-232-858-62
15	447	27.4	401	2	US-09-338-063A-62
16	445	27.2	272	2	US-10-232-858-75
17	445	27.2	272	2	US-09-338-063A-75
18	445	27.2	321	2	US-10-232-858-80
19	445	27.2	321	2	US-09-338-063A-80
20	445	27.2	327	2	US-10-232-858-72
21	445	27.2	327	2	US-09-338-063A-72
22	445	27.2	351	2	US-10-232-858-74
23	445	27.2	351	2	US-09-338-063A-74
24	445	27.2	393	2	US-10-232-858-79
25	445	27.2	393	2	US-09-338-063A-79
26	445	27.2	399	2	US-10-232-858-73
27	445	27.2	399	2	US-09-338-063A-73

28	445	27.2	401	2	US-10-232-858-5	Sequence 5, Appli
29	445	27.2	401	2	US-10-232-858-64	Sequence 64, Appli
30	445	27.2	401	2	US-10-232-858-65	Sequence 65, Appli
31	445	27.2	401	2	US-10-232-858-66	Sequence 66, Appli
32	445	27.2	401	2	US-09-338-063A-5	Sequence 5, Appli
33	445	27.2	401	2	US-09-338-063A-64	Sequence 64, Appli
34	445	27.2	401	2	US-09-338-063A-65	Sequence 65, Appli
35	445	27.2	401	2	US-09-338-063A-66	Sequence 66, Appli
36	444	27.2	293	2	US-09-896-096A-18	Sequence 18, Appli
37	444	27.2	362	2	US-10-232-858-11	Sequence 11, Appli
38	444	27.2	362	2	US-09-338-063A-11	Sequence 11, Appli
39	444	27.2	401	2	US-08-974-022-6	Sequence 6, Appli
40	444	27.2	401	2	US-09-042-785A-12	Sequence 12, Appli
41	444	27.2	401	2	US-08-795-445A-6	Sequence 6, Appli
42	444	27.2	401	2	US-08-795-447A-6	Sequence 6, Appli
43	444	27.2	401	2	US-08-974-186-6	Sequence 6, Appli
44	444	27.2	401	2	US-08-795-446B-6	Sequence 6, Appli
45	444	27.2	401	2	US-09-159-927-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-794-796-2
; Sequence 2, Application US/08794796
; Patent No. 5885800
; GENERAL INFORMATION:
; APPLICANT: Emery, John
; APPLICANT: Tan, KB
; APPLICANT: Truneh, Alem
; APPLICANT: Young, Peter
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,
; TITLE OF INVENTION: TR4
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,796
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: GH50000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 300 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-794-796-2
Query Match 100.0%; Score 1634; DB 1; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.8e-127;

Result No.	Score	Query Match	Length	DB	ID	Description	
1	1634	100.0	300	3	US-09-696-096A-1	Sequence 1, Appli	
2	1634	100.0	300	3	US-09-694-924-1	Sequence 1, Appli	
3	1634	100.0	300	3	US-09-935-727-2	Sequence 2, Appli	
4	1634	100.0	300	4	US-10-129-709-3	Sequence 3, Appli	
5	1634	100.0	300	4	US-10-125-985-2	Sequence 6, Appli	
6	1634	100.0	300	4	US-10-310-793-6	Sequence 6, Appli	
7	1634	100.0	300	4	US-10-369-300-19	Sequence 19, Appli	
8	1634	100.0	300	4	US-10-375-680-52	Sequence 52, Appli	
9	1634	100.0	300	4	US-10-418-242-2	Sequence 2, Appli	
10	1634	100.0	300	4	US-10-456-819-1	Sequence 1, Appli	
11	1634	100.0	300	4	US-10-793-269-2	Sequence 2, Appli	
12	1634	100.0	300	4	US-10-668-132-1	Sequence 1, Appli	
13	1634	100.0	300	4	US-10-466-786-3	Sequence 3, Appli	
14	1634	100.0	300	5	US-10-871-907-1	Sequence 1, Appli	
15	1634	100.0	300	5	US-10-775-180-145	Sequence 145, App	
16	1634	100.0	300	5	US-10-775-180-151	Sequence 151, App	
17	1634	100.0	300	5	US-10-775-180-157	Sequence 157, App	
18	1634	100.0	300	5	US-10-775-180-158	Sequence 158, App	
19	1634	100.0	300	5	US-10-943-197-49	Sequence 49, Appli	
20	1634	100.0	300	5	US-10-775-204-439	Sequence 439, App	
21	1634	100.0	300	5	US-10-775-204-452	Sequence 452, App	
22	1634	100.0	300	5	US-10-775-204-491	Sequence 491, App	
23	1634	100.0	300	5	US-10-775-204-494	Sequence 494, App	
24	1634	100.0	341	4	US-10-106-698-4514	Sequence 4514, Ap	
25	1634	100.0	885	5	US-10-775-180-88	Sequence 88, Appli	
26	1634	100.0	885	5	US-10-775-180-89	Sequence 89, Appli	
27	1634	100.0	885	5	US-10-775-204-275	Sequence 275, App	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2005, 22:36:25 ; Search time 46 Seconds
(without alignments)
539.189 Million cell updates/sec

Title: US-09-518-931-2
Perfect score: 1634
Sequence: 1 MRALGPGLSLCLVALPA.....RVARMPGLSVRFLPVH 300

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2.6/prodata/1/iaa/5_COMB.pep.*
2: /cgn2.6/prodata/1/iaa/6_COMB.pep.*
3: /cgn2.6/prodata/1/iaa/H_COMB.pep.*
4: /cgn2.6/prodata/1/iaa/PTUS_COMB.pep.*
5: /cgn2.6/prodata/1/iaa/RE_COMB.pep.*
6: /cgn2.6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1634	100.0	300	1	US-08-794-796-2
2	1634	100.0	300	2	US-09-632-277A-2
3	1634	100.0	300	2	US-09-523-323-52
4	1634	100.0	300	2	US-09-896-096A-1
5	1634	100.0	300	2	US-09-936-019-3
6	1634	100.0	333	2	US-09-949-016-7678
7	1619.5	99.1	239	2	US-09-286-529-17
8	1491	91.2	271	2	US-09-936-019-1
9	1177	72.0	211	2	US-09-286-529-20
10	855	52.3	146	2	US-09-523-323-59
11	841	51.5	153	2	US-09-286-529-2
12	465.5	28.5	326	2	US-10-232-858-71
13	465.5	28.5	326	2	US-09-338-063A-71
14	447	27.4	401	2	US-10-232-858-62
15	447	27.4	401	2	US-09-338-063A-62
16	445	27.2	272	2	US-10-232-858-75
17	445	27.2	272	2	US-09-338-063A-75
18	445	27.2	321	2	US-10-232-858-80
19	445	27.2	321	2	US-09-338-063A-80
20	445	27.2	327	2	US-10-232-858-72
21	445	27.2	327	2	US-09-338-063A-72
22	445	27.2	351	2	US-10-232-858-74
23	445	27.2	351	2	US-09-338-063A-74
24	445	27.2	393	2	US-10-232-858-79
25	445	27.2	393	2	US-09-338-063A-79
26	445	27.2	399	2	US-10-232-858-73
27	445	27.2	399	2	US-09-338-063A-73

28	445	27.2	401	2	US-10-232-858-5	Sequence 5, Appli
29	445	27.2	401	2	US-10-232-858-64	Sequence 64, Appl
30	445	27.2	401	2	US-10-232-858-65	Sequence 65, Appl
31	445	27.2	401	2	US-10-232-858-66	Sequence 66, Appl
32	445	27.2	401	2	US-09-338-063A-5	Sequence 5, Appli
33	445	27.2	401	2	US-09-338-063A-64	Sequence 64, Appl
34	445	27.2	401	2	US-09-338-063A-65	Sequence 65, Appl
35	445	27.2	401	2	US-09-338-063A-66	Sequence 66, Appl
36	444	27.2	293	2	US-09-896-096A-18	Sequence 18, Appl
37	444	27.2	362	2	US-10-232-858-11	Sequence 11, Appl
38	444	27.2	362	2	US-09-338-063A-11	Sequence 6, Appli
39	444	27.2	401	2	US-08-974-022-6	Sequence 12, Appl
40	444	27.2	401	2	US-09-042-785A-12	Sequence 6, Appli
41	444	27.2	401	2	US-08-795-445A-6	Sequence 6, Appli
42	444	27.2	401	2	US-08-795-447A-6	Sequence 6, Appli
43	444	27.2	401	2	US-08-974-186-6	Sequence 6, Appli
44	444	27.2	401	2	US-08-795-446B-6	Sequence 1, Appli
45	444	27.2	401	2	US-09-153-927-1	

ALIGNMENTS

RESULT 1
US-08-794-796-2
; Sequence 2, Application US/08794796
; Patent No. 5885800
; GENERAL INFORMATION:
; APPLICANT: Emery, John
; APPLICANT: Tan, KB
; APPLICANT: Truneh, Alem
; APPLICANT: Young, Peter
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,
; TITLE OF INVENTION: TR4
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,796
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: GH50000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 300 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-794-796-2

Query Match 100.0%; Score 1634; DB 1; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.8e-127;